M	T	E	T	A	Y	G	N	A	Q	D	L	L	V	E	WT-ROS
M	T	E	T	A	Y	G	N	A	Q	D	L	L	V	E	SYNROS
M	T	D	M	A	T	G	N	A	P	E	L	L	V	E	ROS-R
M	T	E	T	A	Y	G	N	A	Q	D	L	L	V	E	ROS-AR
M	T	E	T	S	L	G	T	S	N	E	L	L	V	E	MUC-R
L	T	A	D	I	V	A	A	Y	V	S	N	H	V	V	WT-ROS
L	T	A	D	I	V	A	A	Y	V	S	N	H	V	V	SYNROS
L	T	A	D	I	V	A	A	Y	V	S	N	H	V	V	ROS-R
L	T	A	D	I	V	A	A	Y	V	S	N	H	V	V	ROS-AR
L	T	A	E	I	V	A	A	Y	V	S	N	H	V	V	MUC-R
P	V	T	E	L	P	G	L	I	S	D	V	H	T	A	WT-ROS
P	V	T	E	L	P	G	L	I	S	D	V	H	T	A	SYNROS
P	V	S	D	L	A	N	L	I	S	D	V	H	S	A	ROS-R
P	V	T	E	L	P	G	L	I	S	D	V	H	T	A	ROS-AR
P	V	A	E	L	P	T	L	I	A	D	V	H	S	A	MUC-R
L	S	G	T	S	A	P	A	S	V	A	V	N	V	E	WT-ROS
L	S	G	T	S	A	P	A	S	V	A	V	N	V	E	SYNROS
L	S	N	T	S	V	P	Q	P	A	A	A	V	V	E	ROS-R
L	S	G	T	S	A	P	A	S	V	A	V	N	V	E	ROS-AR
L	N	N	T	T	A	P	A	P	V	V	V	P	V	E	MUC-R
K	Q	K	P	A	V	S	V	R	K	S	V	Q	D	D	WT-ROS
K	Q	K	P	A	V	S	V	R	K	S	V	Q	D	D	SYNROS
K	Q	K	P	A	V	S	V	R	K	S	V	Q	D	E	ROS-R
K	Q	K	P	A	V	S	V	R	K	S	V	Q	D	D	ROS-AR
K	P	K	P	A	V	S	V	R	K	S	V	Q	D	D	MUC-R
H	I	V	C	L	E	C	G	G	S	F	K	S	L	K	WT-ROS
H	I	V	C	L	E	C	G	G	S	F	K	S	L	K	SYNROS
Q	I	T	C	L	E	C	G	G	N	F	K	S	L	K	ROS-R
H	I	V	C	L	E	C	G	G	S	F	K	S	L	K	ROS-AR
Q	I	T	C	L	E	C	G	G	T	F	K	S	L	K	MUC-R
R	H	L	T	T	H	H	S	M	T	P	E	E	Y	R	WT-ROS
R	H	L	T	T	H	H	S	M	T	P	E	E	Y	R	SYNROS
R	H	L	M	T	H	H	S	L	S	P	E	E	Y	R	ROS-R
R	H	L	T	T	H	H	S	M	T	P	E	E	Y	R	ROS-AR
R	H	L	M	T	H	H	N	L	S	P	E	E	Y	R	MUC-R
E	K	W	D	L	P	V	D	Y	P	M	V	A	P	A	WT-ROS
E	K	W	D	L	P	V	D	Y	P	M	V	A	P	A	SYNROS
E	K	W	D	L	P	T	D	Y	P	M	V	A	P	A	ROS-R
E	K	W	D	L	Q	V	D	Y	P	M	V	A	P	A	ROS-AR
D	K	W	D	L	P	A	D	Y	P	M	V	A	P	A	MUC-R
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G	WT-ROS
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G	SYNROS
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G	ROS-R
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G	ROS-AR
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G	MUC-AR
Q	R	R	K	A	N	R									WT-ROS
Q	R	R	K	A	N	R	P	K	K	K	R	K	V		SYNROS
Q	R	R	K	R	G	R	G								ROS-R
Q	R	R	K	A	N	R									ROS-AR
Q	R	R	K	R	R	G	K								MUC-AR

FIG. 1A

GCGGATCCCC GGGTATGACT GAGACTGCTT ACGGTAACGC
TCAGGATCTT CTTGTTGAGC TTACTGCTGA TATCGTTGCT
GCTTACGTTT CTAACCACGT TGTTCCTGTT ACTGAGCTTC
CTGGACTTAT CTCTGATGTT CATACTGCAC TTTCTGGAAC
ATCTGCTCCT GCTTCTGTTG CTGTTAACGT TGAGAAGCAG
AAGCCTGCTG TTTCTGTTCG TAAGTCTGTT CAGGATGATC
ATATCGTTTG TTTGGAGTGT GGTGGTTCTT TCAAGTCTCT
CAAGCGTCAC CTTACTACTC ATCACTCTAT GACTCCAGAG
GAGTATAGAG AGAAGTGGGA TCTTCCTGTT GATTACCCTA
TGGTTGCTCC TGCTTACGCT GAGGCTCGTT CTCGTCTCGC
TAAGGAGATG GGTCTCGGTC AGCGTCGTAA GGCTAACCGT
CCAAAAAAGA AGCGTAAGGT CTGAGAGCTC GC

FIG. 1B

M	T	E	T	A	Y	G	N	A	Q	D	L	L	V	E
ATG	ACN	GAR	ACN	GCN	TAY	GGN	AAY	GCN	CAR	GAY	YTN	YTN	GTN	GAR
L	T	A	D	I	V	A	A	Y	V	S	N	H	V	V
YTN	ACN	GCN	GAY	ATH	GTN	GCN	GCN	TAY	GTN	WSN	AAY	CAY	GTN	GTN
P	V	T	E	L	P	G	L	I	S	D	V	H	T	A
CCN	GTN	ACN	GAR	YTN	CCN	GGN	YTN	ATH	WSN	GAY	GTN	CAY	ACN	GCN
L	S	G	T	S	A	P	A	S	V	A	V	N	V	E
YTN	WSN	GGN	ACN	WSN	GCN	CCN	GCN	WSN	GTN	GCN	GTN	AAY	GTN	GAR
K	Q	K	P	A	V	S	V	R	K	S	V	Q	D	D
AAR	CAR	AAR	CCN	GCN	GTN	WSN	GTN	MGN	AAR	WSN	GTN	CAR	GAY	GAY
H	I	V	C	L	E	C	G	G	S	F	K	S	L	K
CAY	ATH	GTN	TGY	YTN	GAR	TGY	GGN	GGN	WSN	TTY	AAR	WSN	YTN	AAR
R	H	L	T	T	H	H	S	M	T	P	E	E	Y	R
MGN	CAY	YTN	ACN	ACN	CAY	CAY	WSN	ATG	ACN	CCN	GAR	GAR	TAY	MGN
E	K	W	D	L	P	V	D	Y	P	M	V	A	P	A
GAR	AAR	TGG	GAY	YTN	CCN	GTN	GAY	TAY	CCN	ATG	GTN	GCN	CCN	GCN
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G
TAY	GCN	GAR	GCN	MGN	WSN	MGN	YTN	GCN	AAR	GAR	ATG	GGN	YTN	GGN
Q	R	R	K	A	N	R	*P*	*K*	*K*	*K*	*R*	*K*	*V*	
CAR	MGN	MGN	AAR	GCN	AAY	MGN	*CCN*	*AAR*	*AAR*	*AAR*	*MGN*	*AAR*	*GTN*	

FIG. 1C

ROS Inverted Repeat
DNA Binding Sites(Operator sequences)

TATATTTCAA-TTTTA-**TTGTAATATA** *virC/virD*
**** ** ** * *** *** **
TATAATTAAAATATTAA**CTGTCGCATT** *ipt*

FIG. 1D

Comparison of ROS DNA Binding Site (Operator) Sequences

VirC/VirD	**TATATTTCAA**
	TATATTACAA
ipt	**TATAATTAAA**
	AATGCGACAG
	TATAHTtCAA
	a g gaa g
Consensus	**WATDHWKMAR**

FIG. 1E

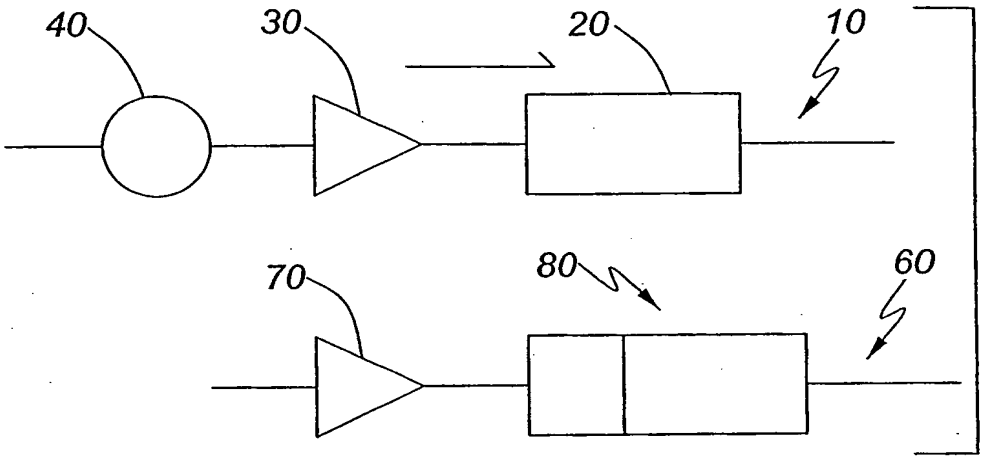


FIG. 2A

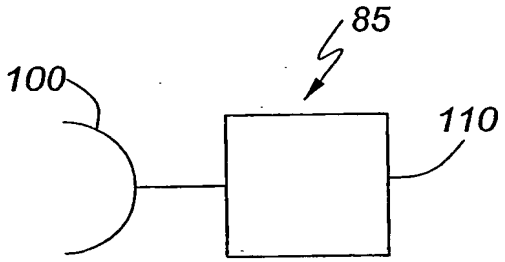


FIG. 2B

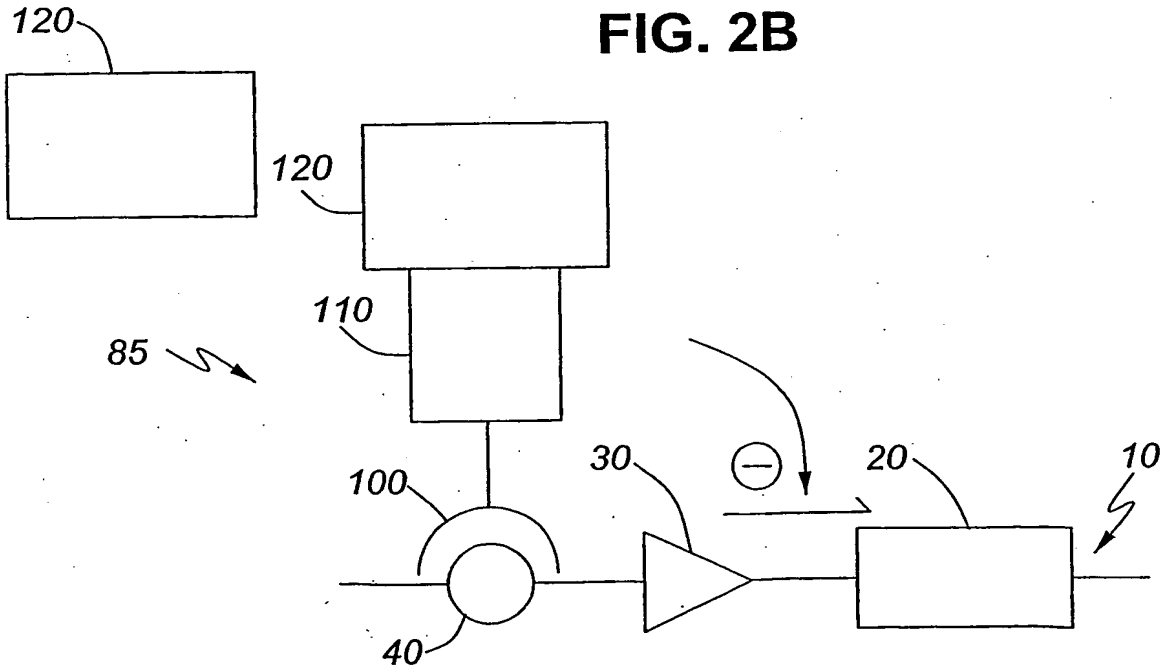


FIG. 2C

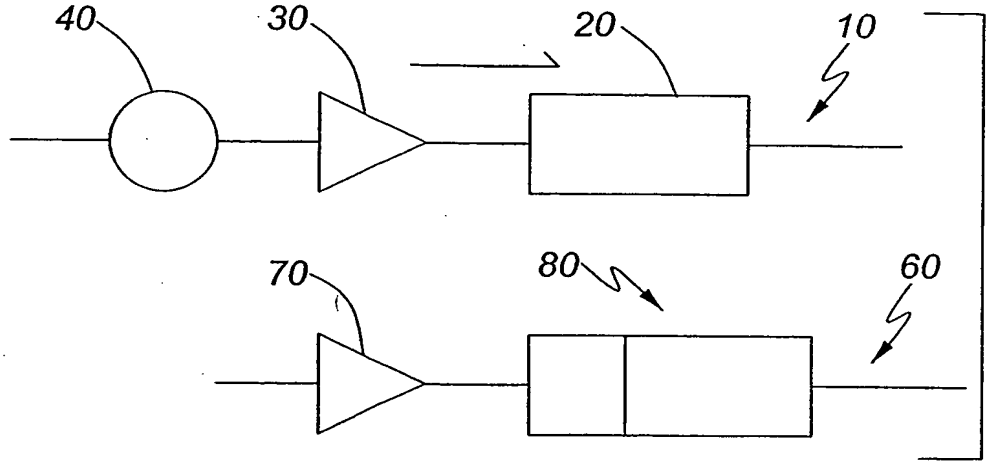


FIG. 3A

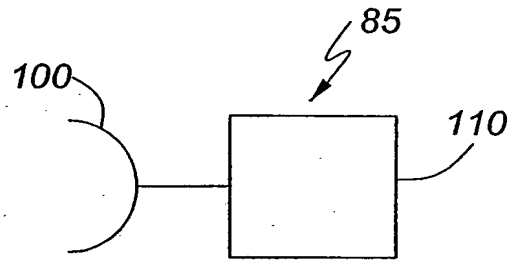


FIG. 3B

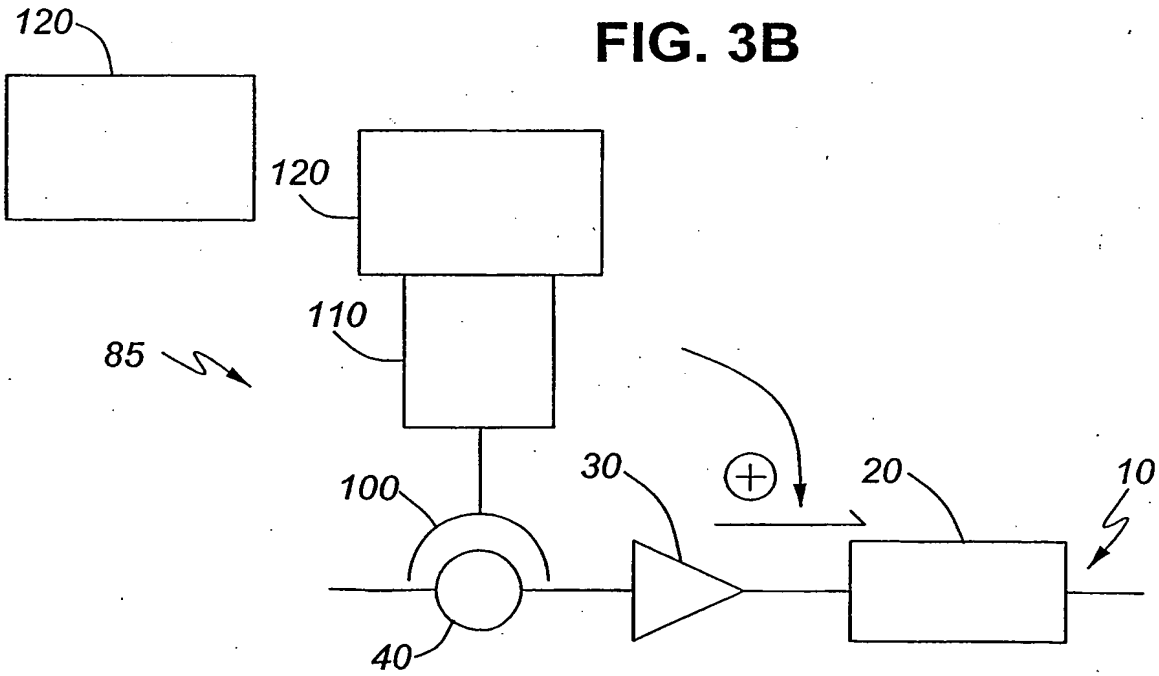


FIG. 3C

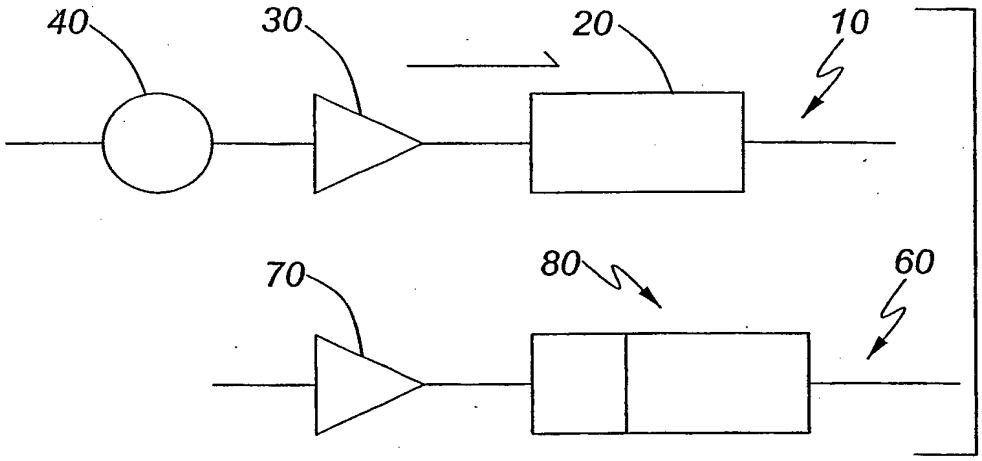


FIG. 4A

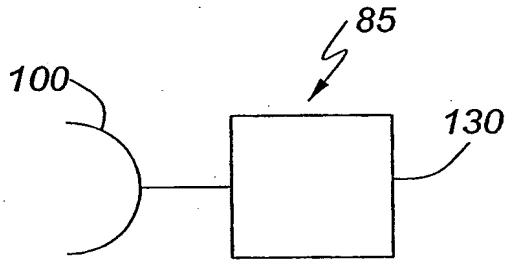


FIG. 4B

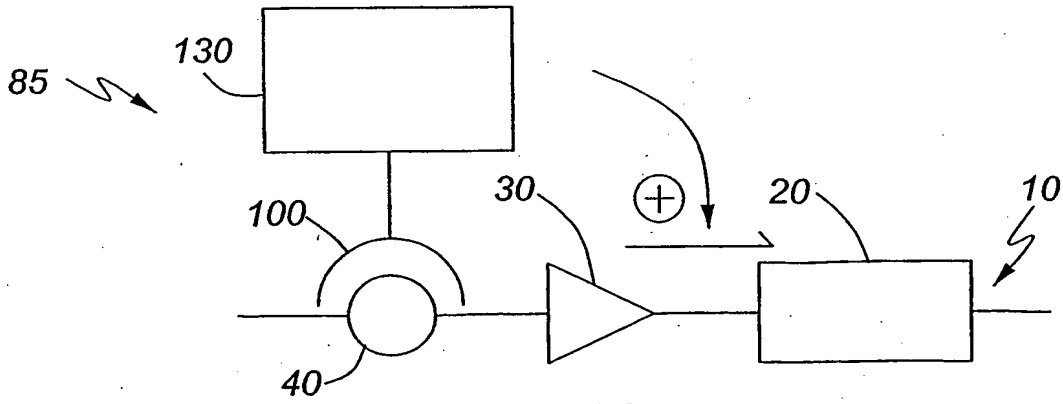
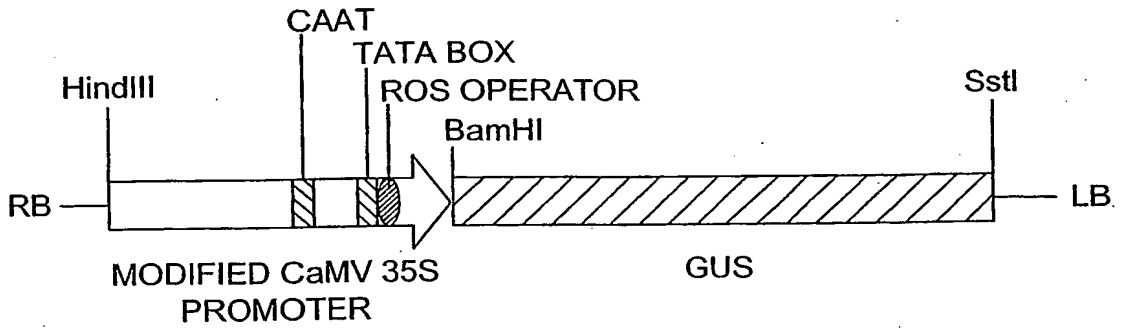


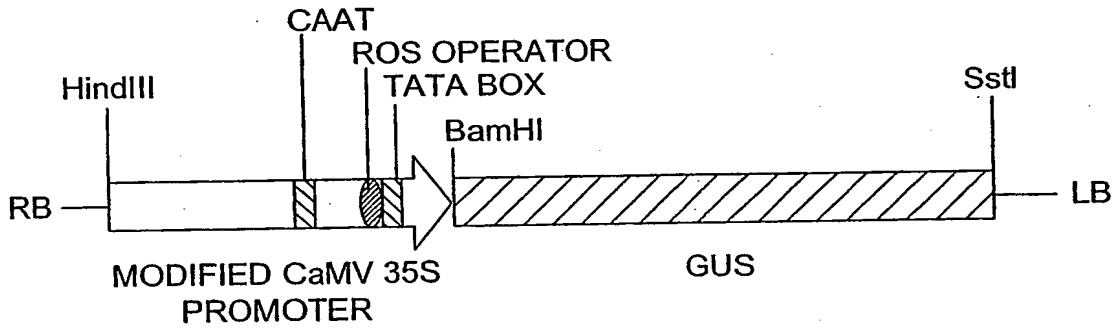
FIG. 4C

8/36



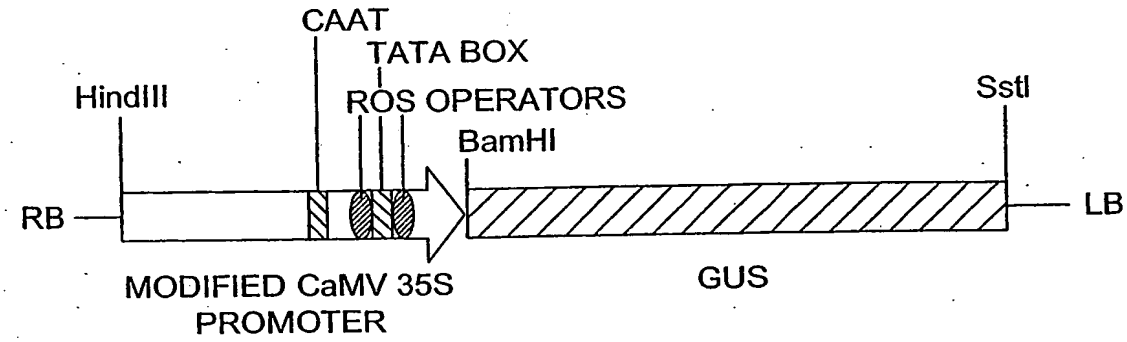
p74-315

FIG. 5A



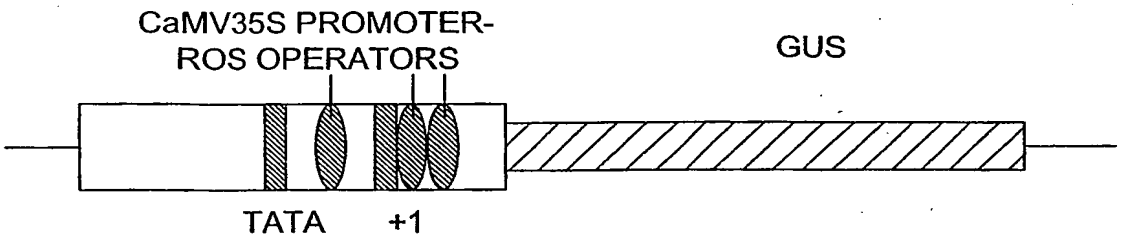
p74-316

FIG. 5B



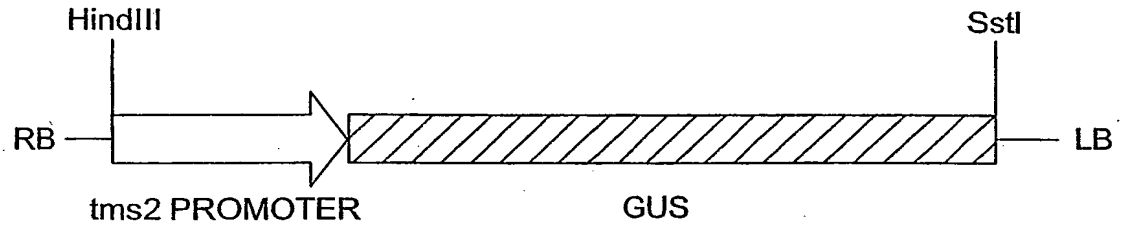
p74-309

FIG. 5C



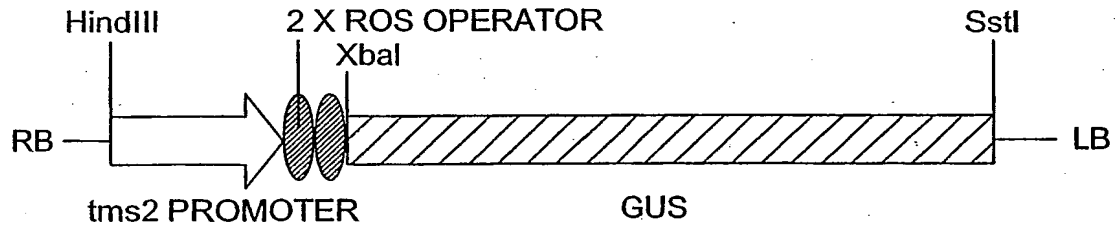
p74-118

FIG. 5D



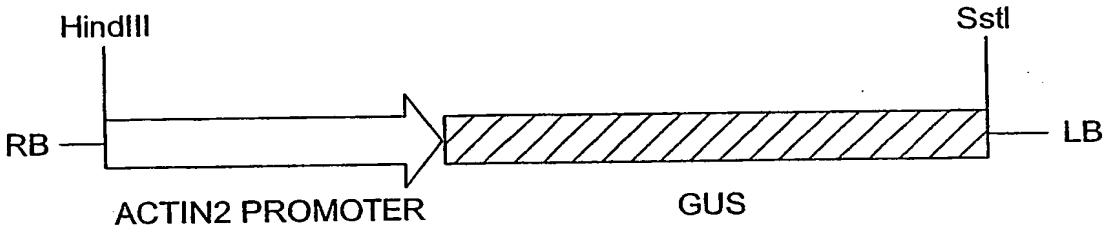
p76-507

FIG. 6A



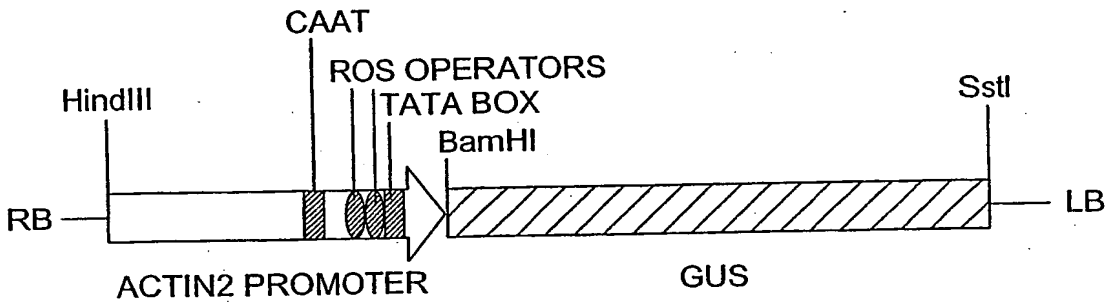
p76-508

FIG. 6B



p75-101

FIG. 7A



p74-501

FIG. 7B

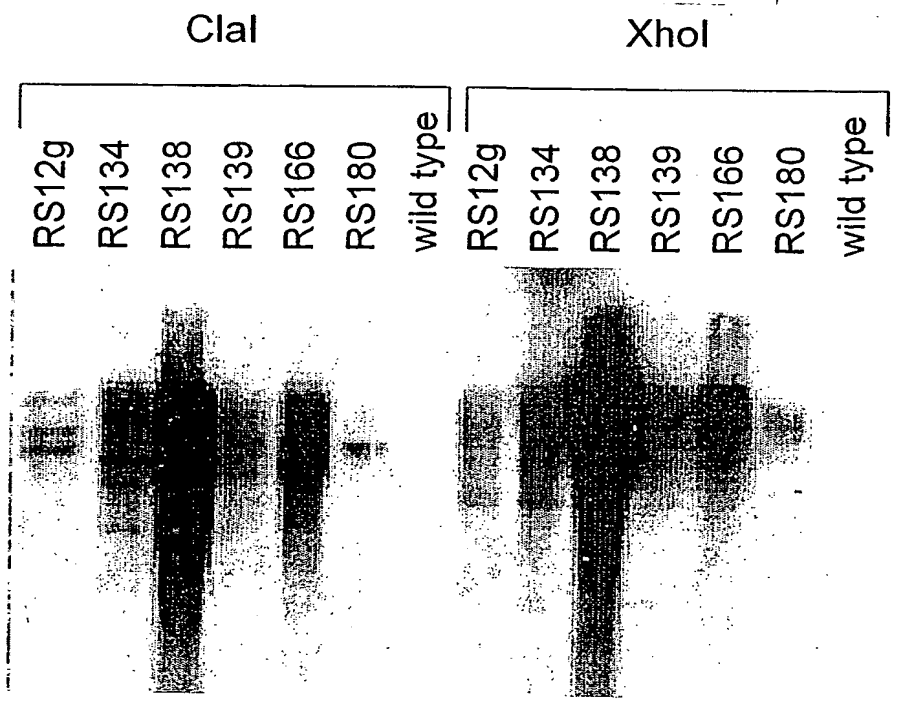

ClaI
XhoI
RS12g
RS134
RS138
RS139
RS166
RS180
wild type
RS12g
RS134
RS138
RS139
RS166
RS180
wild type

FIG. 8A

P74-101

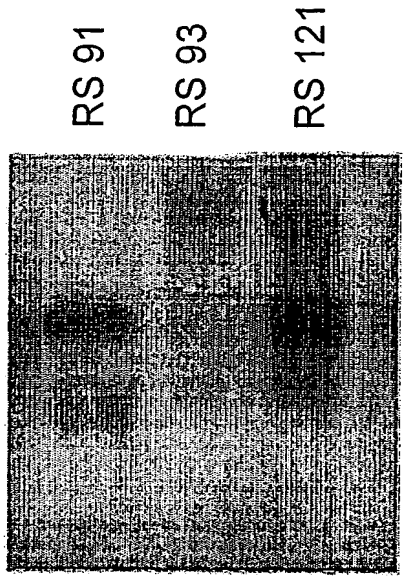


FIG. 8B

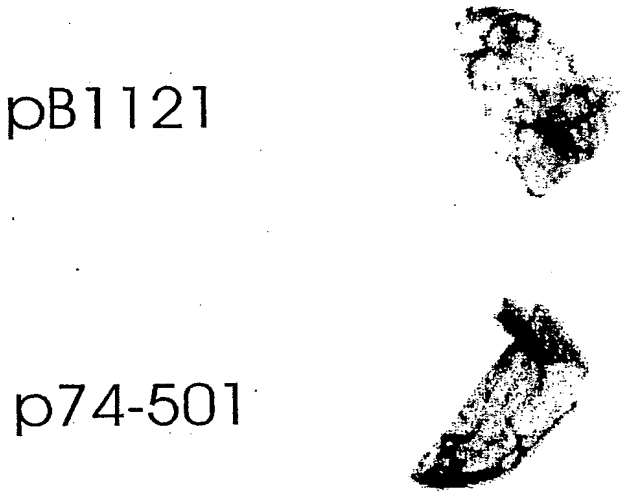


FIG. 9

```
bnKCP     (1)  M-AGGGPTFSIELSAYG-SDLPTDKASGDIP------NEEGSGLSRVGSGIW
atKCP     (1)  MELMAKPTFSIEVSQYGTTDLPATEKASSSSSSFETTNEEG-VEESGLSRIW
atKCL1    (1)  M--------EVLVGSTFRDRSSVTTHDQAVP--------AS-LSSRIGLRRC
atKCL2    (1)  M---VGSSFGIGMAAYVRDHRGVSAQDKAVQTALFLADESGRGGSQIGIGLR

bnKCP    (45)  SG----RTVDYSSESSSSIGTPGDSEEEDEESEEDNDEEEL------GLASL
atKCP    (52)  SG----QTADYSSDSSS-IGTPGDSEEDEEESENENDDVSSKELGLRGLASM
atKCL1   (36)  GR-------SPPPESSSSVGETSENEEDEDDAVSSSQGRWLN-------SFS
atKCL2   (50)  MSNNNNKSPEESSDSSSSIGESSENEEEEEEDDAVSCQRGTLD------SFS

                                                          ********
bnKCP    (87)  RSLEDSLPSK-GLSSHYKGKSKSFGNLGEIG-SVKEVPKQENPLNKKRRLQI
atKCP    (99)  SSLEDSLPSKRGLSNHYKGKSKSFGNLGEIG-SVKEVAKQENPLNKRRRLQI
atKCL1   (74)  SSLEDSLPIKRGLSNHYIGKSKSFGNLMEAS-NTNDLVKVESPLNKRRRLLI
atKCL2   (96)  SSLEDSLPIKRGLSNHYVGKSKSFGNLMEAASKAKDLEKVENPFNKRRRLVI

bnKCP   (137)  YNKLARKS------FYSWQNPKSMPLLPVHEDNDDEEGDDG-----------
atKCP   (150)  CNKLARKS------FYSWQNPKSMPLLPVNEDEDDDDEDDDEEDLKSGFDEN
atKCL1  (125)  ANKLRRRSSLSSFSIYTKINPNSMPLLALQESDNEDHKLNDDDDDDDS---S
atKCL2  (148)  ANKLRRR-------------GRSITYEEDHHIHNDDYEDDDG----------

                                  ◇◇◇◇
bnKCP   (172)  -DLSDEERGGDVLARRPSFKNRALKSMSCFALSDLQEEEE----EEEDE
atKCP   (196)  KSSSDEEGVKKVVVRKGSFKNRAYKSRSCFALSDLIEEED----DDDDQ
atKCL1  (174)  SDDETSKLKEKRMKMTNHRDFMVPQTKSCFSLTSFQDDDDR--------
atKCL2  (177)  ----DGDDHRKIMMMMKNKKELMAQTRSCFCLSSLQEEDDGDGDDDEDE
```

FIG. 10A

Fig. 10B

```
                                ****
bnKCP    GDDGDLSDEERGGDVLARRPSFKNRALKSMSCFALSDLQEEE
ATF-1    DSSDSIGSSQQAHGILARRPSYRKILKDLSSEDTRGRKGDGE
hyCREB   ESVDSVTDSQKRREILSRRPSYRKILNDLSSDAPGVPRIEEE
CREB     ESVDSVTDSQKRREILSRRPSYRKILNDLSSDAPGVPRIEEE
CREM     SADSEVIDSHKRREILSRRPSYRKILNELSSDVPGIPKIEEE
cCREM    AESEGVIDSHKRREILSRRPSYRKILNELSSDVPGVPKIEEE
```

Fig. 10C

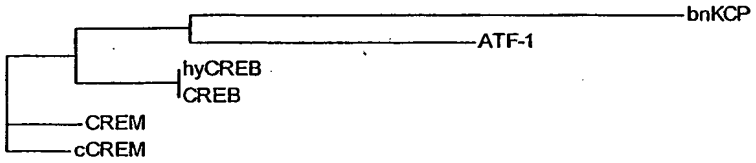


FIG. 10

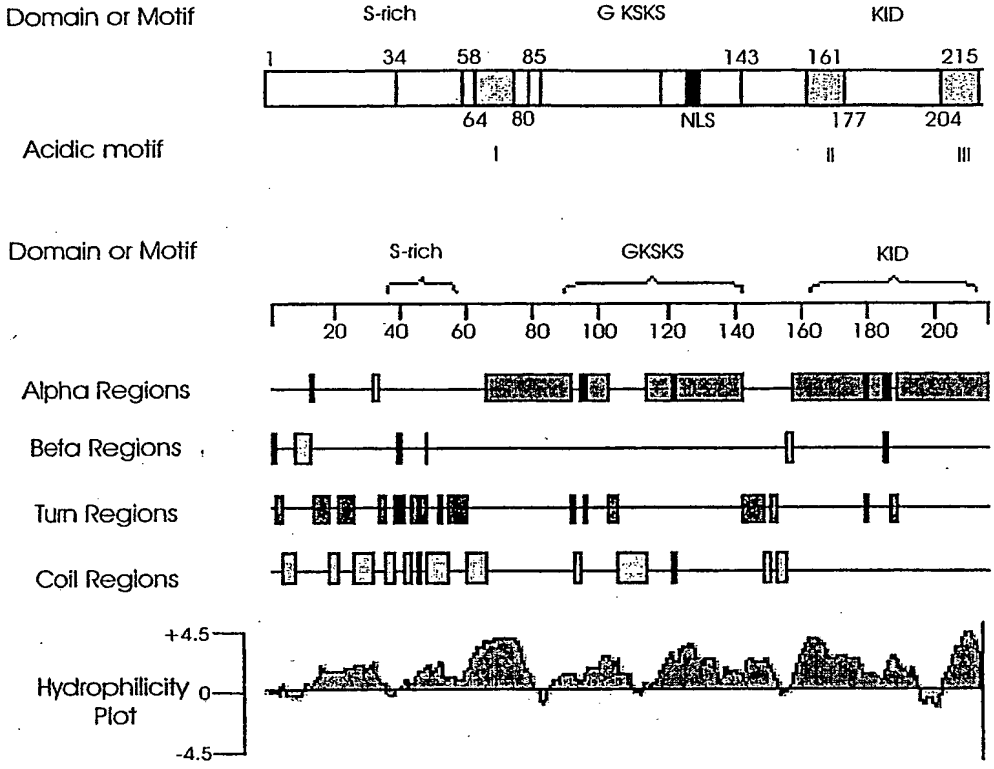

Domain or Motif
S-rich
G KSKS
KID
1
34
58
85
143
161
215
64
80
NLS
177
204
Acidic motif
I
II
III
Domain or Motif
S-rich
GKSKS
KID
20
40
60
80
100
120
140
160
180
200
Alpha Regions
Beta Regions
Turn Regions
Coil Regions
+4.5
Hydrophilicity Plot
0
-4.5

FIG. 11

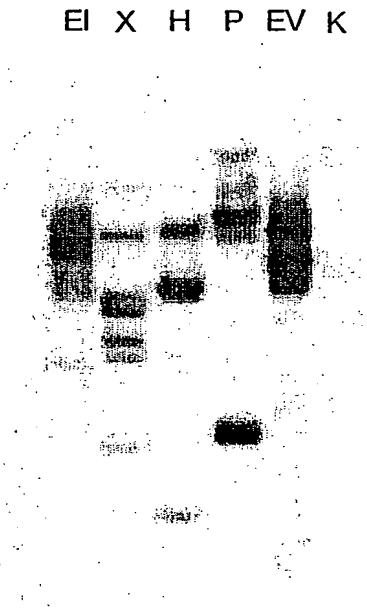


FIG. 12

Fig. 13A

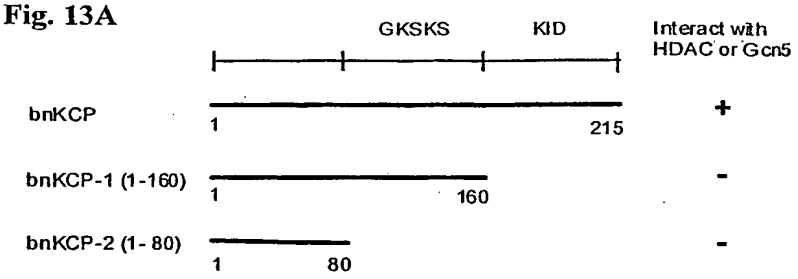


Fig. 13B

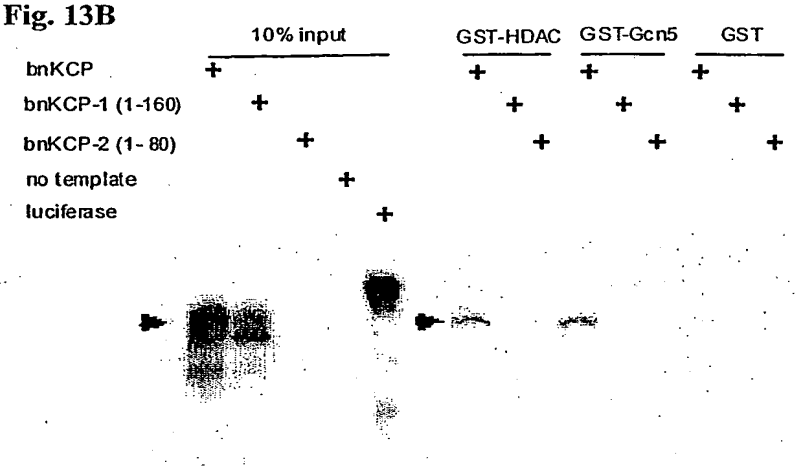


FIG. 13

Fig. 13C-1

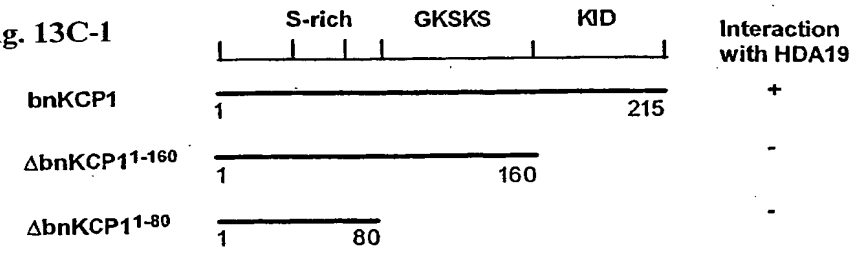


Fig. 13C-2

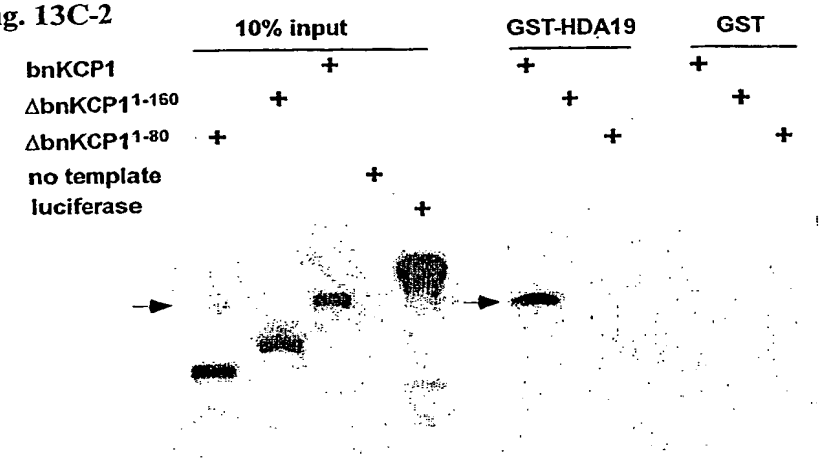


Fig. 13C-3

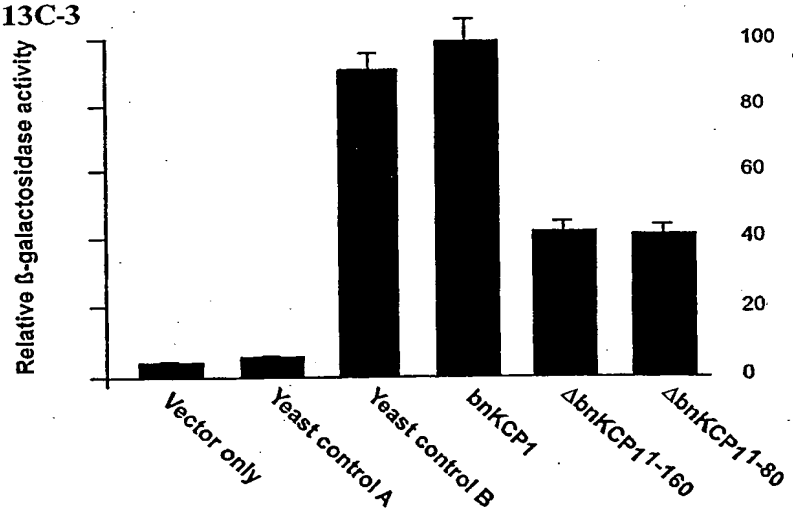


FIG. 13 cont'd

Fig. 14A

Wild type KID (RRPS^{188}) GDDGDLSDEERGGDVLARRPSFKNRALKSMSCFALSDLQEEE

Mutant KID (RRPG^{188}) GDDGDLSDEERGGDVLARRPGFKNRALKSMSCFALSDLQEEE

Fig. 14B

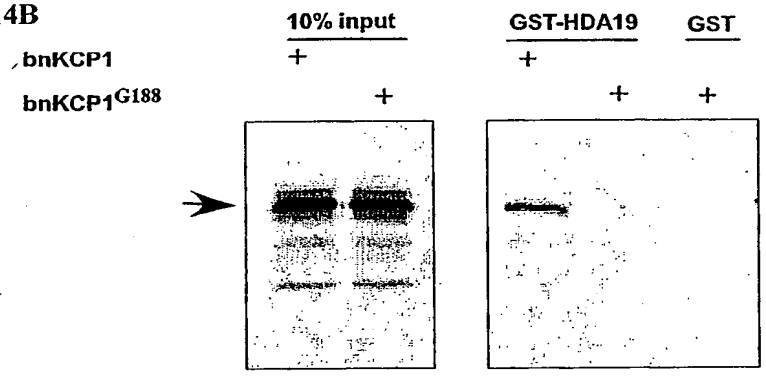


FIG. 14

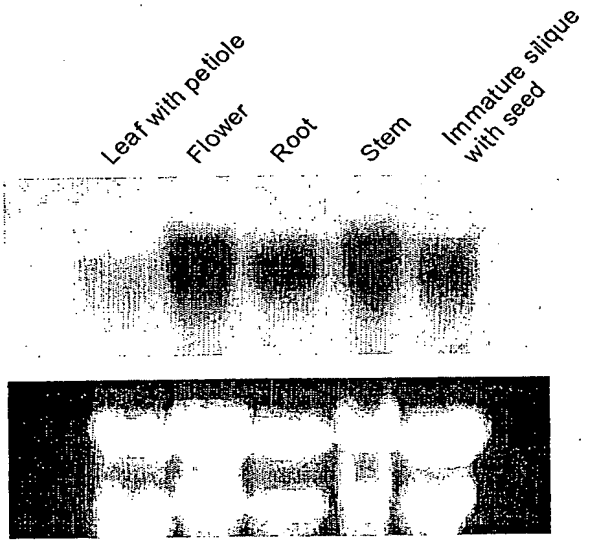

Leaf with petiole
Flower
Root
Stem
Immature silique with seed

FIG. 15

Fig. 16A

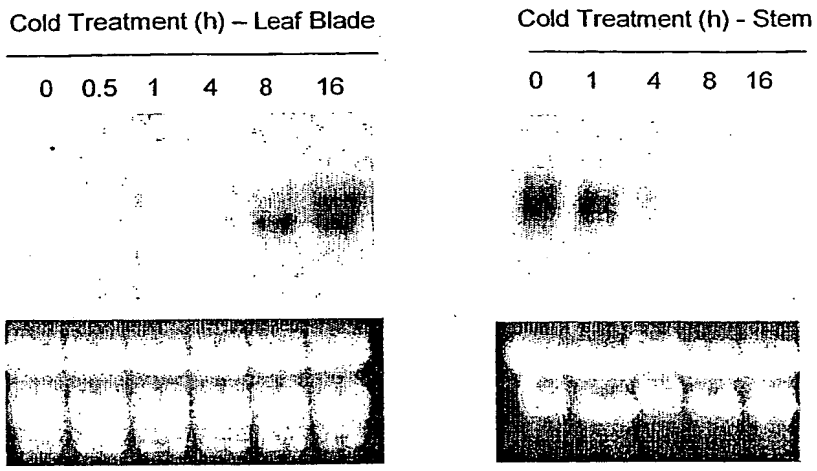


Fig. 16B

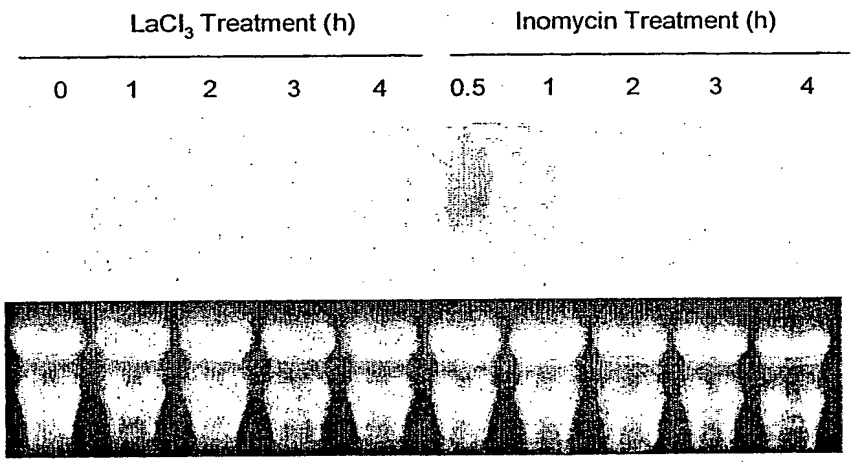


FIG. 16

Fig. 17A

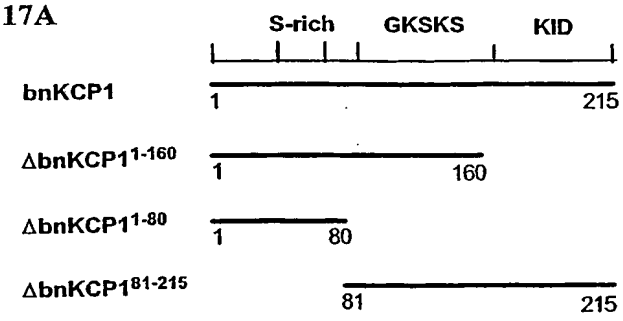


Fig. 17B

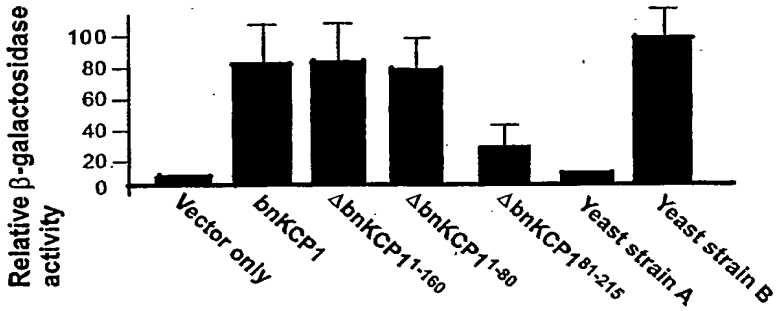


FIG. 17

Fig. 18A

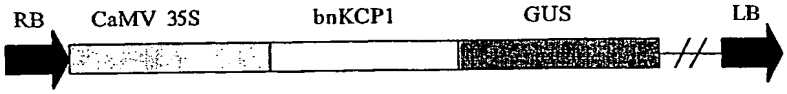


Fig. 18B

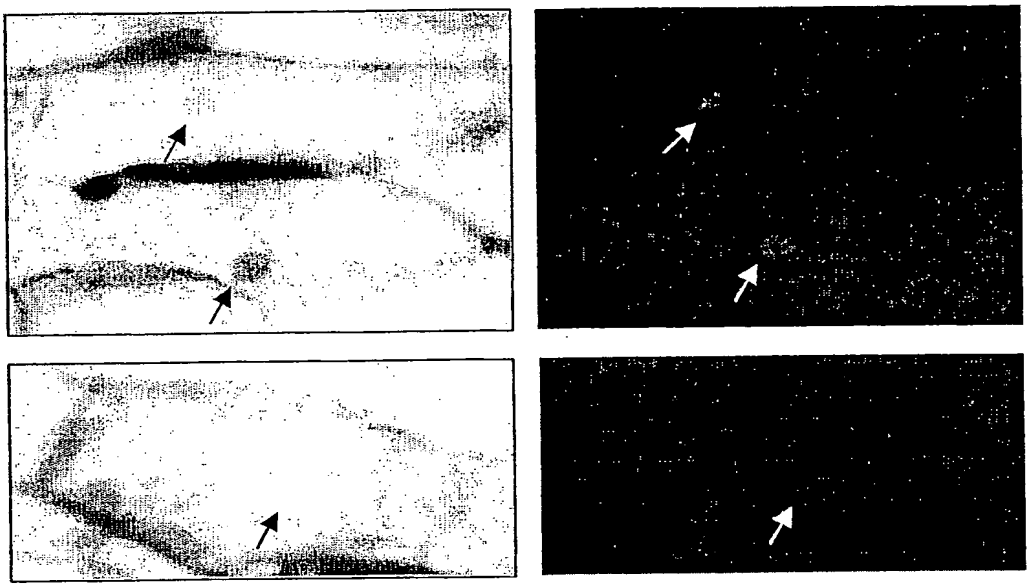


FIG. 18

Strategy for cloning zinc finger domain fusion with KID

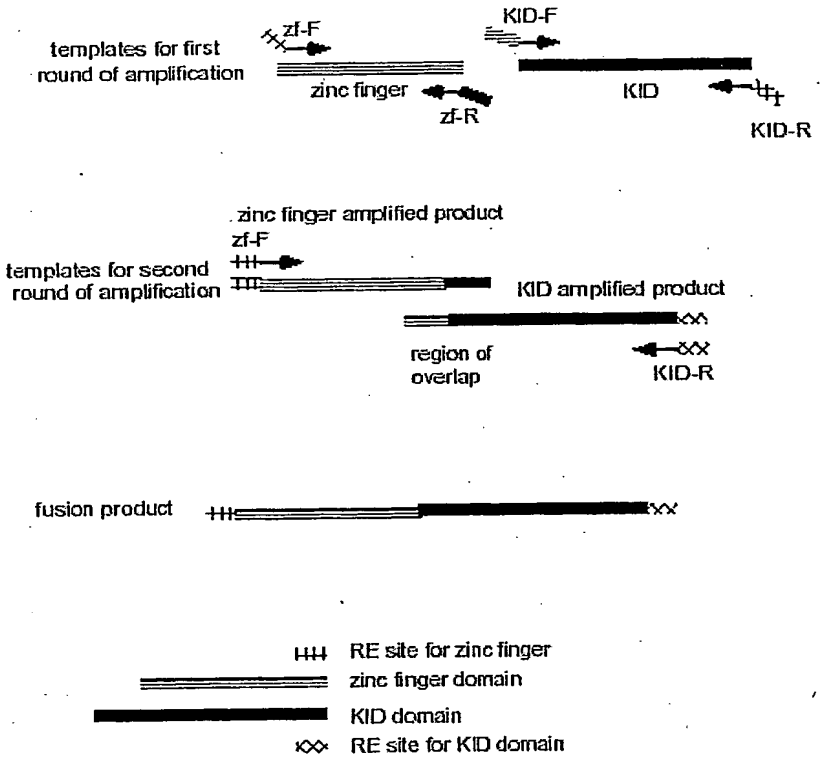


FIG. 19

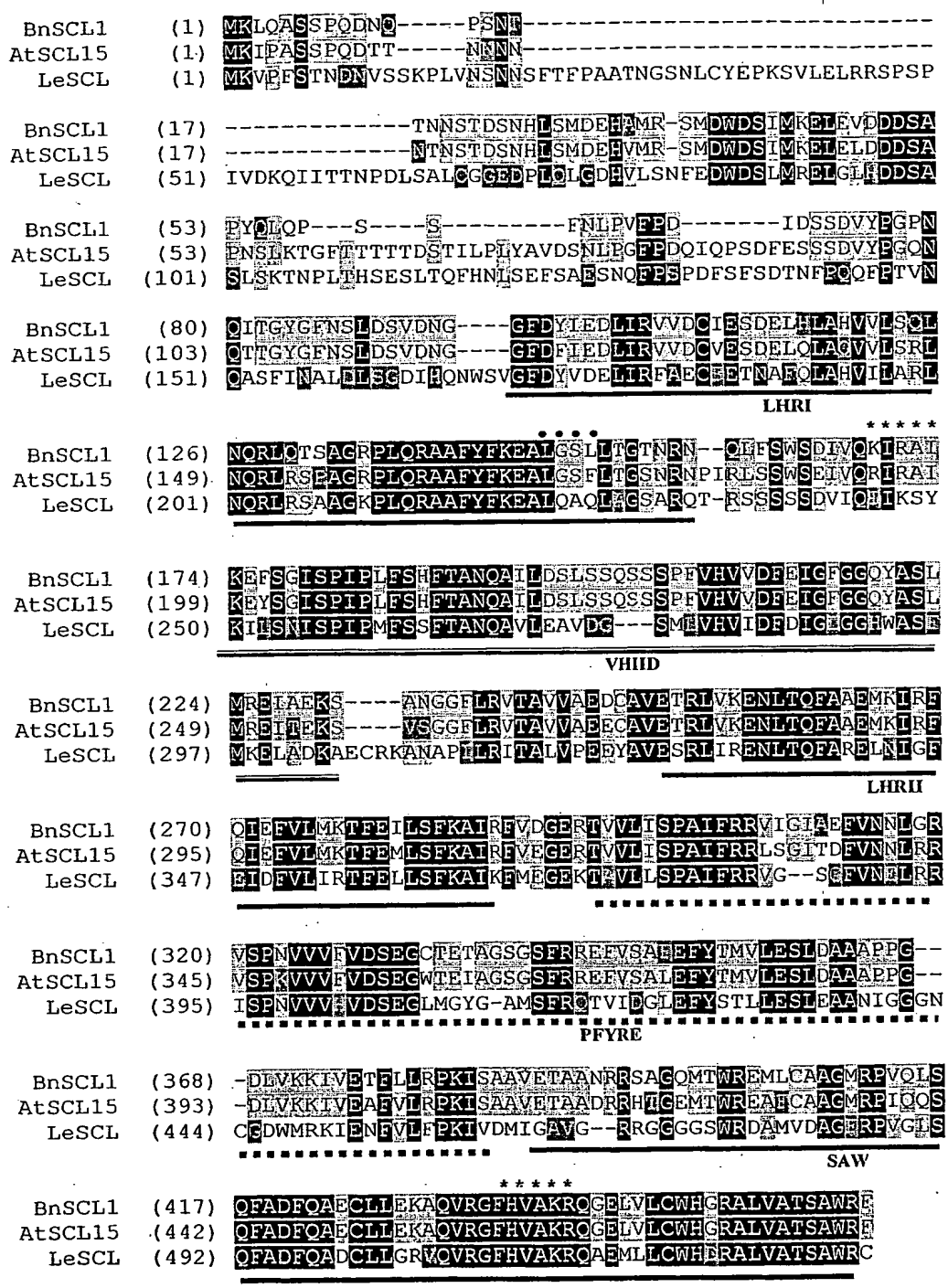

BnSCL1 (1) MKLQASSPQDNQ-----PSNT
AtSCL15 (1) MKIPASSPQDTT-----NNNN
LeSCL (1) MKVPFSTNDNVSSKPLVNSNNSFTFPAATNGSNLCYEPKSVLELRRSPSP
BnSCL1 (17) ----------TNNSTDSNHLSMDEHAMR-SMDWDSIMKELEVDDDSA
AtSCL15 (17) ----------NTNSTDSNHLSMDEHVMR-SMDWDSIMKELELDDDSA
LeSCL (51) IVDKQIITTNPDLSALCGGEDPLQLGDHVLSNFEDWDSLMRELGLHDDSA
BnSCL1 (53) PYQLQP---S-----S----------FNLPVFPD--------IDSSDVYPGPN
AtSCL15 (53) PNSLKTGFTTTTTDSTILPLYAVDSNLPGFPDQIQPSDFESSSDVYPGQN
LeSCL (101) SLSKTNPLTHSESLTQFHNLSEFSAESNQFPSPDFSFSDTNFPQQFPTVN
BnSCL1 (80) QITGYGFNSLDSVDNG----GFDYIEDLIRVVDCIESDELHLAHVVLSQL
AtSCL15 (103) QTTGYGFNSLDSVDNG----GFDFIEDLIRVVDCVESDELQLAQVVLSRL
LeSCL (151) QASFINALDLSGDIHQNWSVGFDYVDELIRFAECEETNAEQLAHVILARL
LHRI
BnSCL1 (126) NQRLQTSAGRPLQRAAFYFKEALGSLLTGTNRN--QLFSWSDIVQKIRAI
AtSCL15 (149) NQRLRSEAGRPLQRAAFYFKEALGSFLTGSNRNPIRLSSWSEIVQRIRAI
LeSCL (201) NQRLRSAAGKPLQRAAFYFKEALQAQLAGSARQT-RSSSSSDVIQHIKSY
BnSCL1 (174) KEFSGISPIPLFSHFTANQAILDSLSSQSSSPFVHVVDFEIGFGGQYASL
AtSCL15 (199) KEYSGISPIPLFSHFTANQAILDSLSSQSSSPFVHVVDFEIGFGGQYASL
LeSCL (250) KILSNISPIPMFSSFTANQAVLEAVDG---SMTVHVIDFDIGIGGHWASF
VHIID
BnSCL1 (224) MREIAEKS----ANGGFLRVTAVVAEDCAVETRLVKENLTQFAAEMKIRF
AtSCL15 (249) MREITEKS----VSGGFLRVTAVVAEECAVETRLVKENLTQFAAEMKIRF
LeSCL (297) MKELADKAECRKANAPILRITALVPEDYAVESRLIRENLTQFARELNIGF
LHRII
BnSCL1 (270) QIEFVLMKTFEILSFKAIRFVDGERTVVLISPAIFRRVIGIAEFVNNLGR
AtSCL15 (295) QIEFVLMKTFEMLSFKAIRFVEGERTVVLISPAIFRRLSGITDFVNNLRR
LeSCL (347) EIDFVLIRTFELLSFKAIKEMEGEKTEVLLSPAIFRRVG--SGFVNILRR
BnSCL1 (320) VSPNVVVFVDSEGCTETAGSGSFRREFVSALEFYTMVLESLDAAAPPG--
AtSCL15 (345) VSPKVVVFVDSEGWTEIAGSGSFRREFVSALEFYTMVLESLDAAAPPG--
LeSCL (395) ISPNVVVFVDSEGLMGYG-AMSFRQTVIDGLEFYSTLLESLEAANIGGGN
PFYRE
BnSCL1 (368) -DLVKKIVETFLLRPKISAAVETAANRRSAGQMTWREMLCAAGMRPVQLS
AtSCL15 (393) -DLVKKIVEAFVLRPKISAAVETAADRRHIGEMTWREAFCAAGMRPIQQS
LeSCL (444) CGDWMRKIENFVLFPKIVDMIGAVG--RRGGGGSWRDAMVDAGFRPVGLS
SAW
BnSCL1 (417) QFADFQAECLLEKAQVRGFHVAKRQGELVLCWHGRALVATSAWRE
AtSCL15 (442) QFADFQAECLLEKAQVRGFHVAKRQGELVLCWHGRALVATSAWRE
LeSCL (492) QFADFQADCLLGRVQVRGFHVAKRQAEMLLCWHERALVATSAWRC

FIG. 20

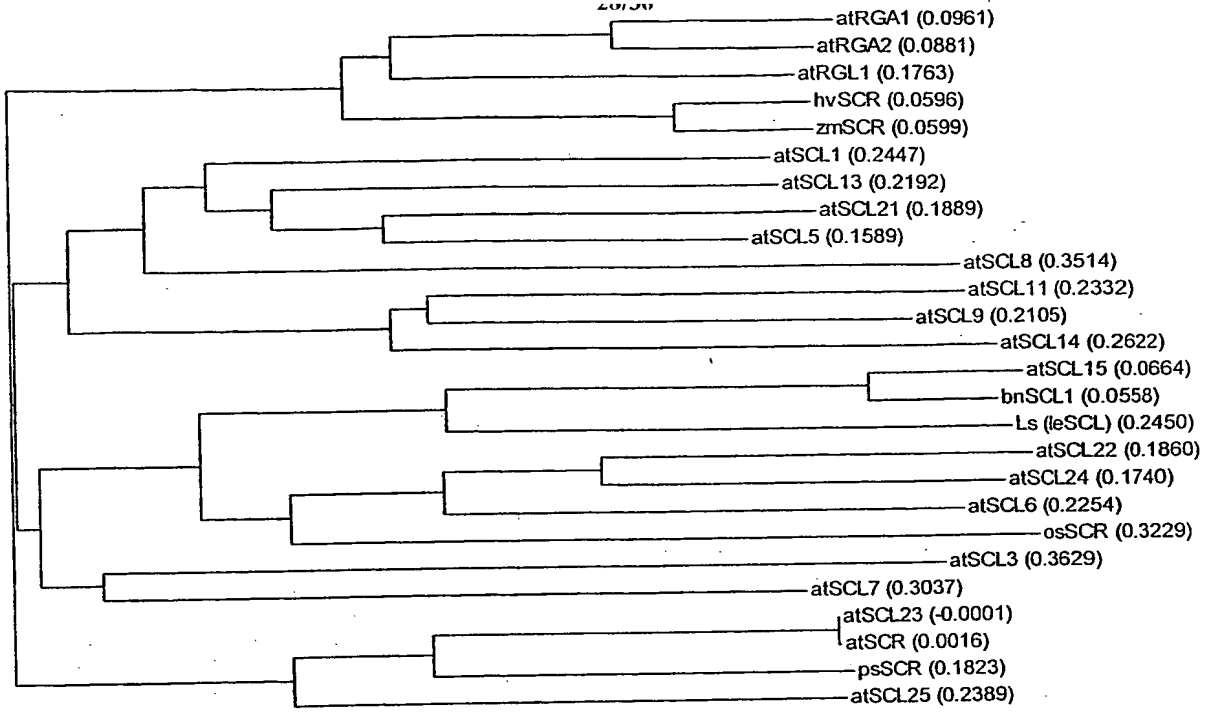

atRGA1 (0.0961)
atRGA2 (0.0881)
atRGL1 (0.1763)
hvSCR (0.0596)
zmSCR (0.0599)
atSCL1 (0.2447)
atSCL13 (0.2192)
atSCL21 (0.1889)
atSCL5 (0.1589)
atSCL8 (0.3514)
atSCL11 (0.2332)
atSCL9 (0.2105)
atSCL14 (0.2622)
atSCL15 (0.0664)
bnSCL1 (0.0558)
Ls (leSCL) (0.2450)
atSCL22 (0.1860)
atSCL24 (0.1740)
atSCL6 (0.2254)
osSCR (0.3229)
atSCL3 (0.3629)
atSCL7 (0.3037)
atSCL23 (-0.0001)
atSCR (0.0016)
psSCR (0.1823)
atSCL25 (0.2389)

FIG. 21

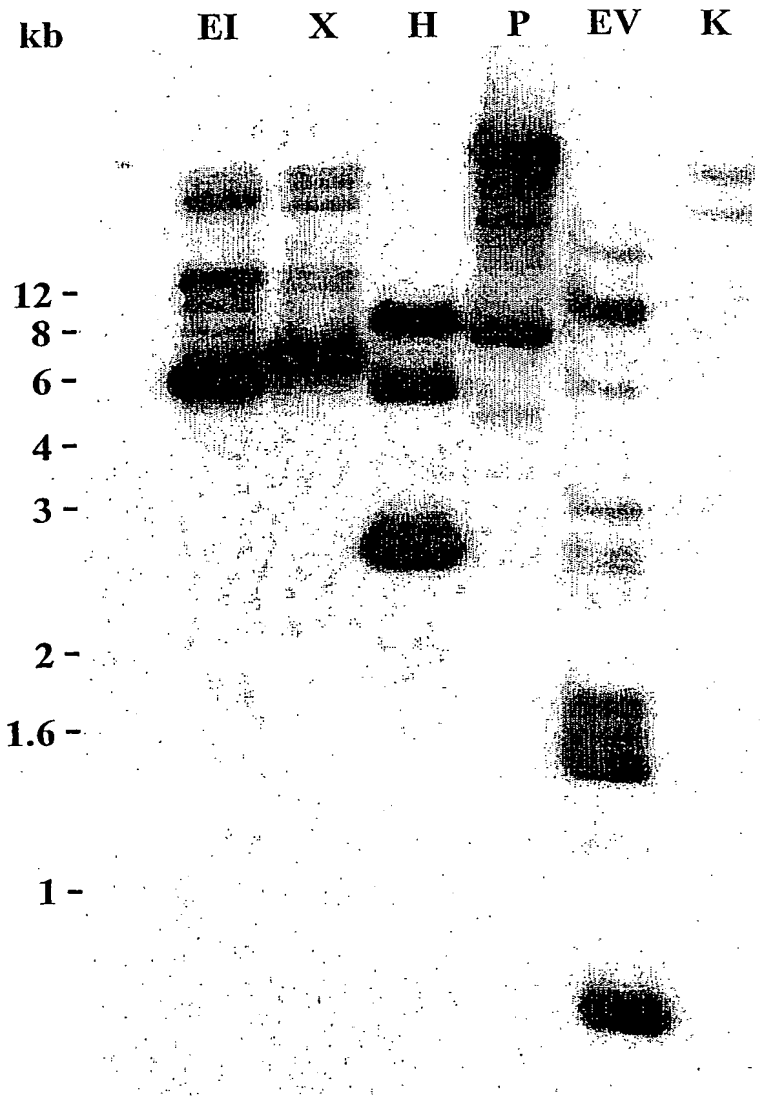


FIG. 22

Fig. 23A

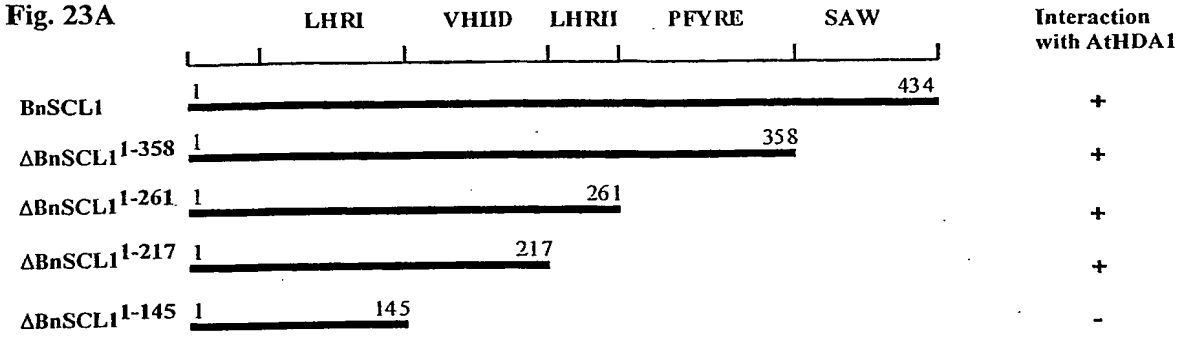


Fig. 23B

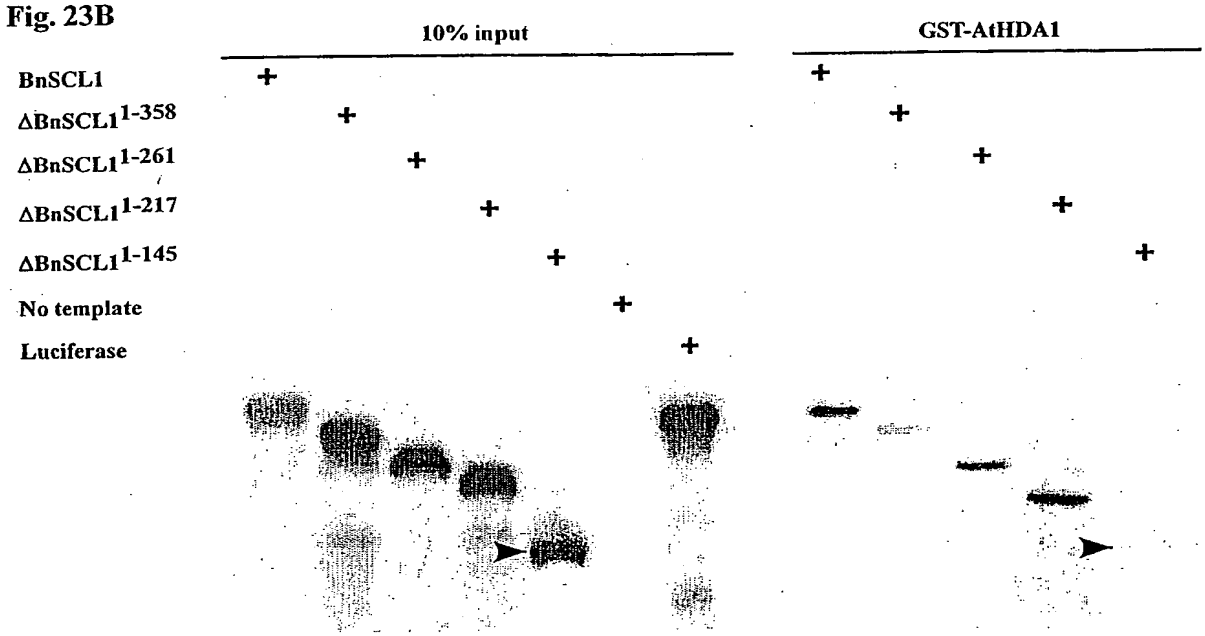


FIG. 23

Fig. 24A

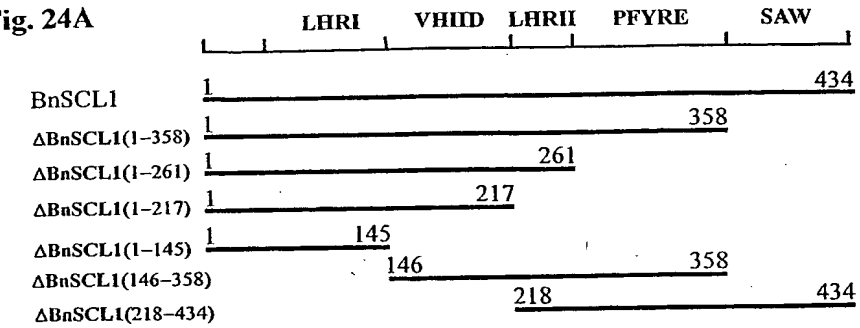


Fig. 24B

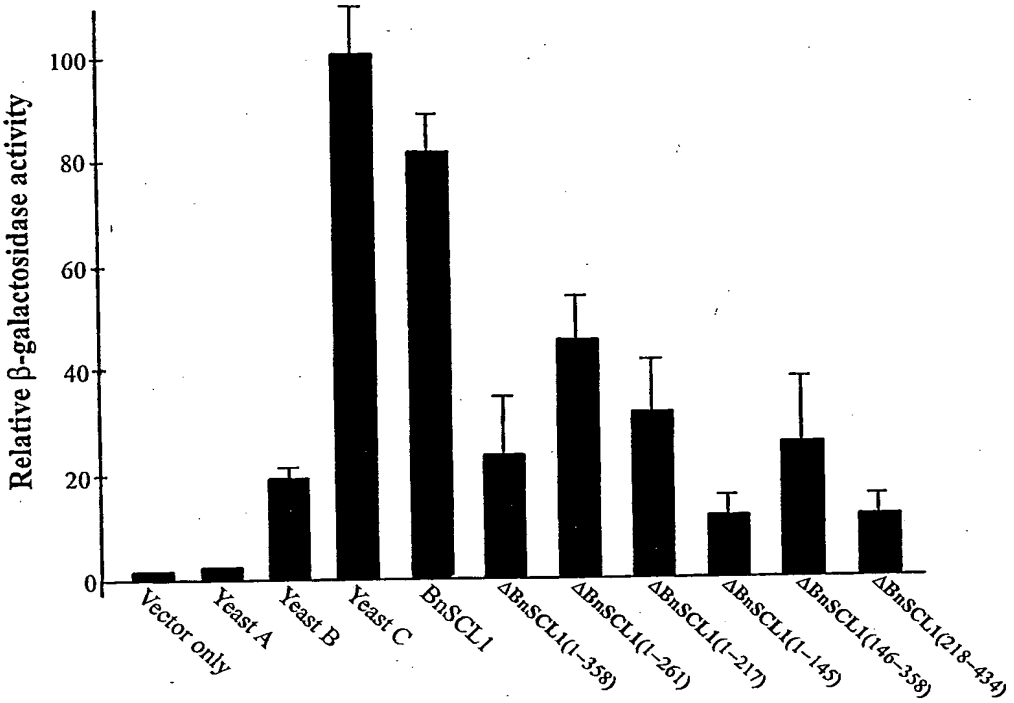


FIG. 24

Fig. 25A

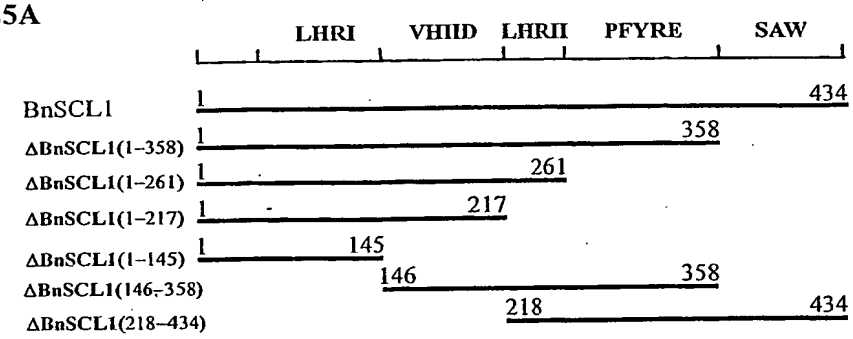


Fig. 25B

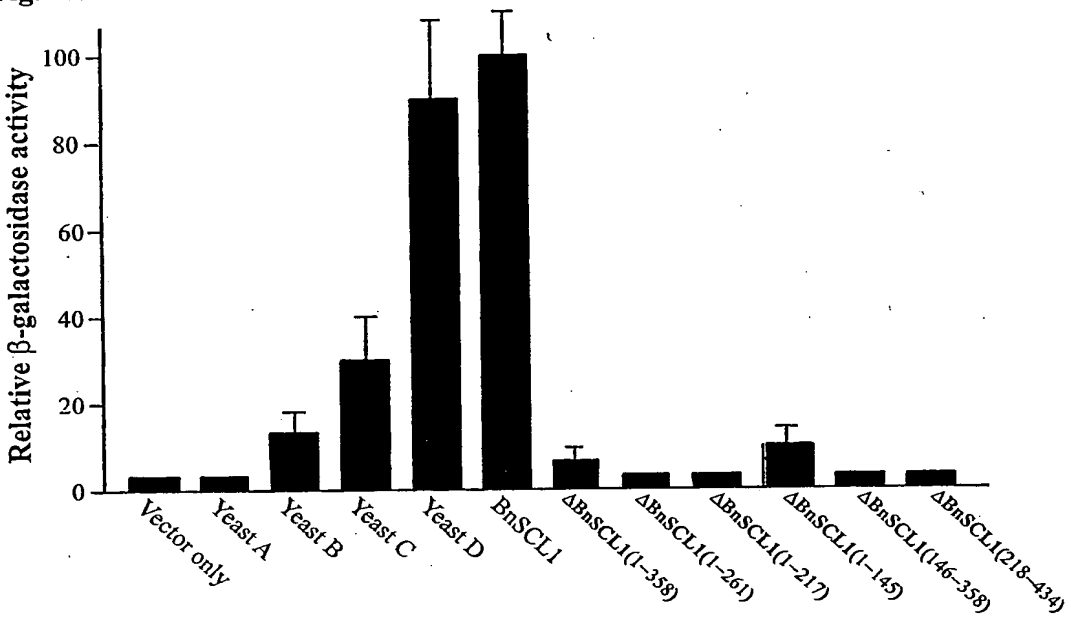


FIG. 25

Fig. 26A

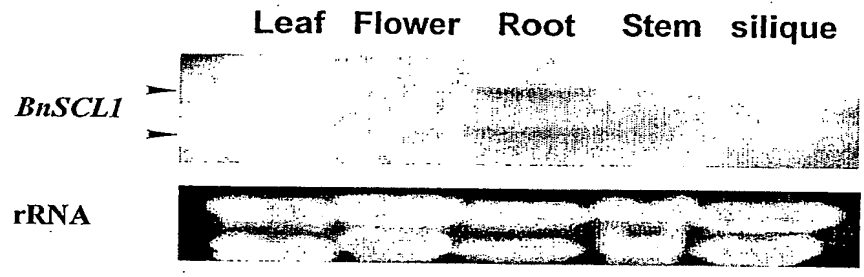


Fig. 26B

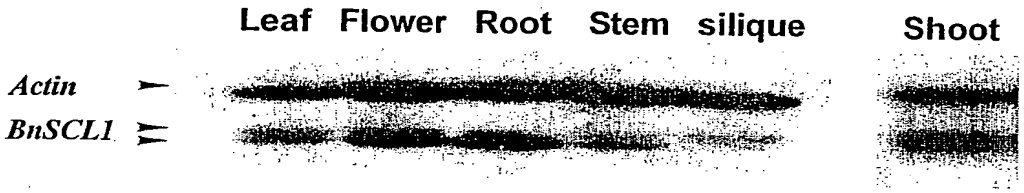


FIG. 26

SUBSTITUTE SHEET (RULE 26)

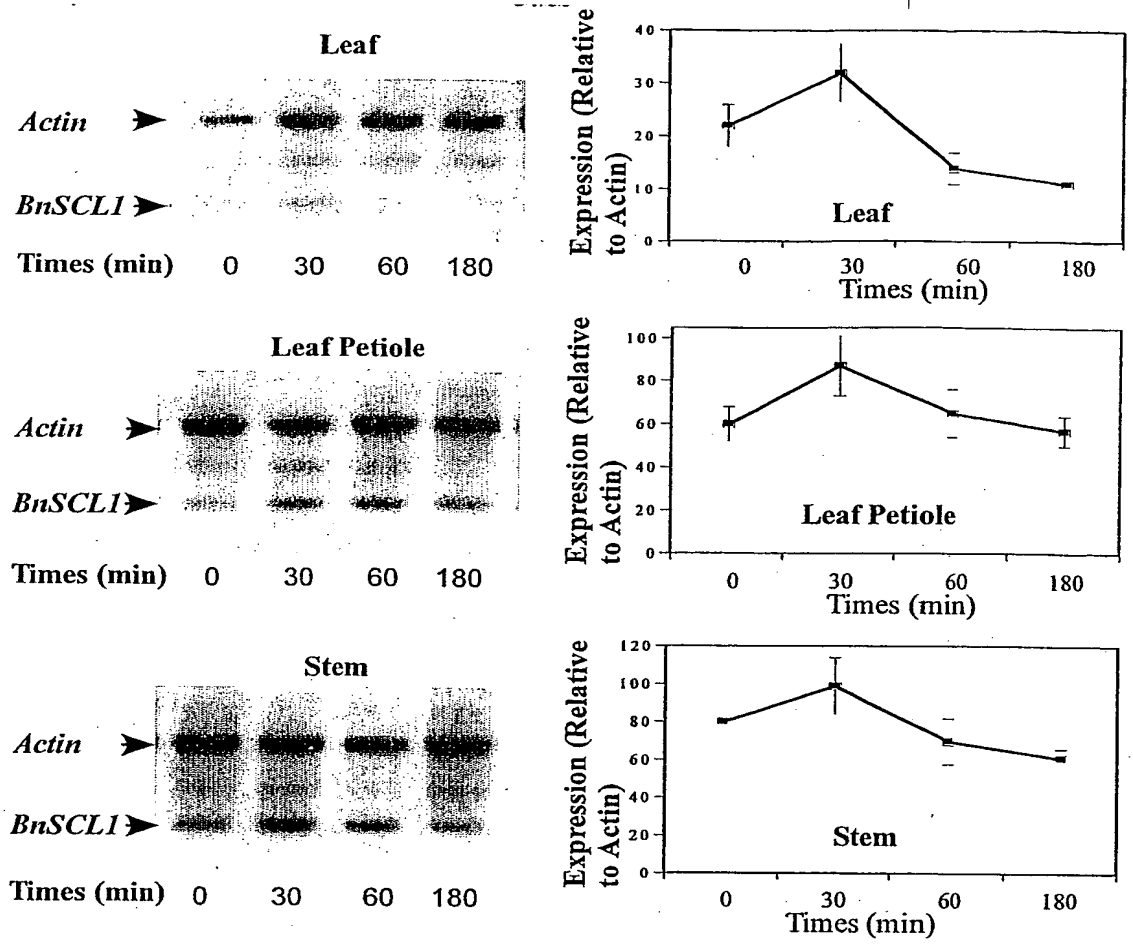

Leaf
Actin
BnSCL1
Times (min) 0 30 60 180
Expression (Relative to Actin)
Leaf
Times (min)
Leaf Petiole
Actin
BnSCL1
Times (min) 0 30 60 180
Expression (Relative to Actin)
Leaf Petiole
Times (min)
Stem
Actin
BnSCL1
Times (min) 0 30 60 180
Expression (Relative to Actin)
Stem
Times (min)

FIG. 27

Fig. 28A

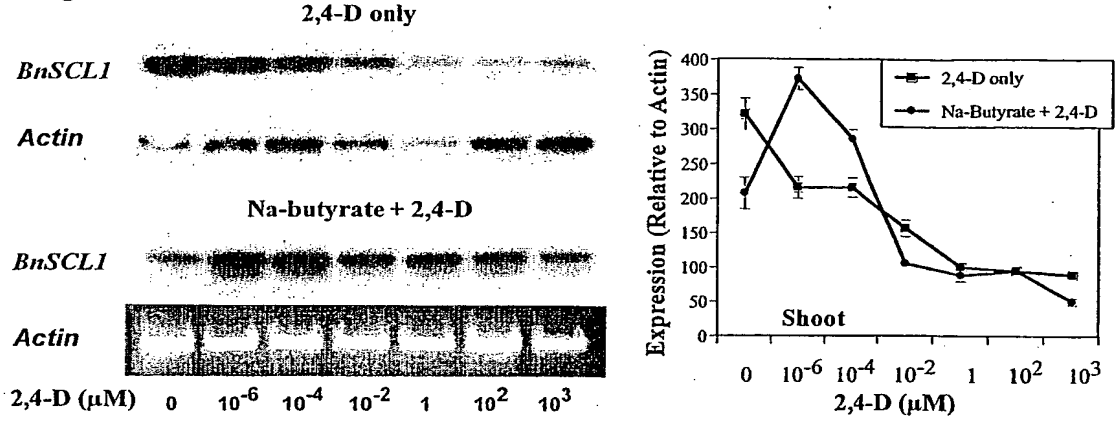


Fig. 28B

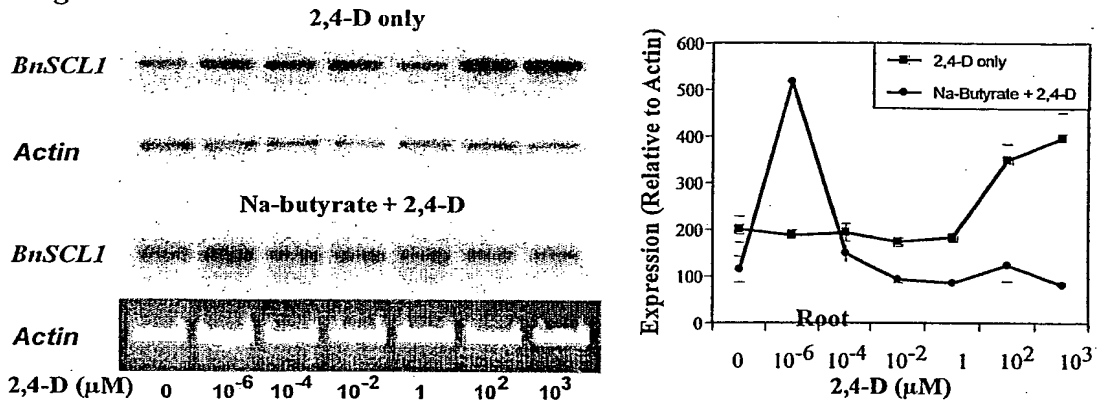


Fig. 28C

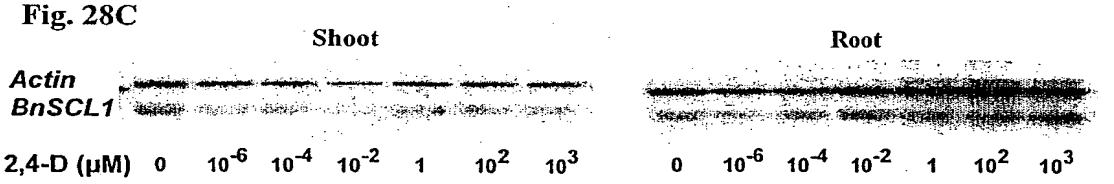


FIG. 28

Fig. 29A

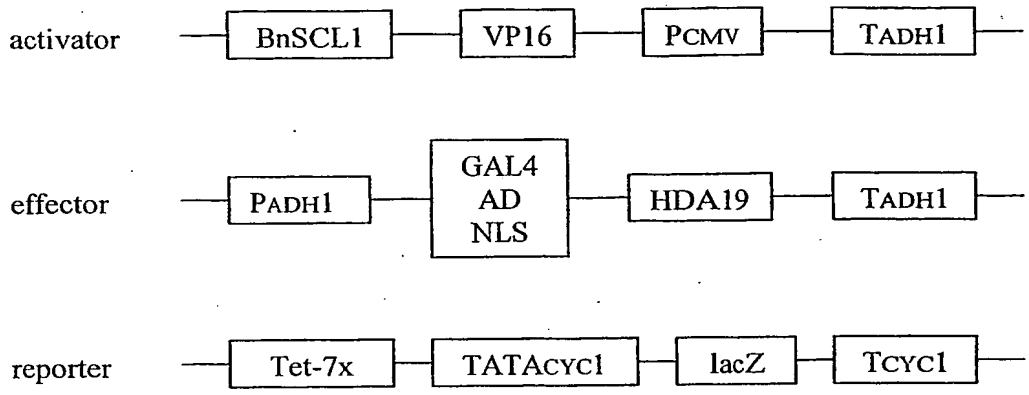


Fig. 29B

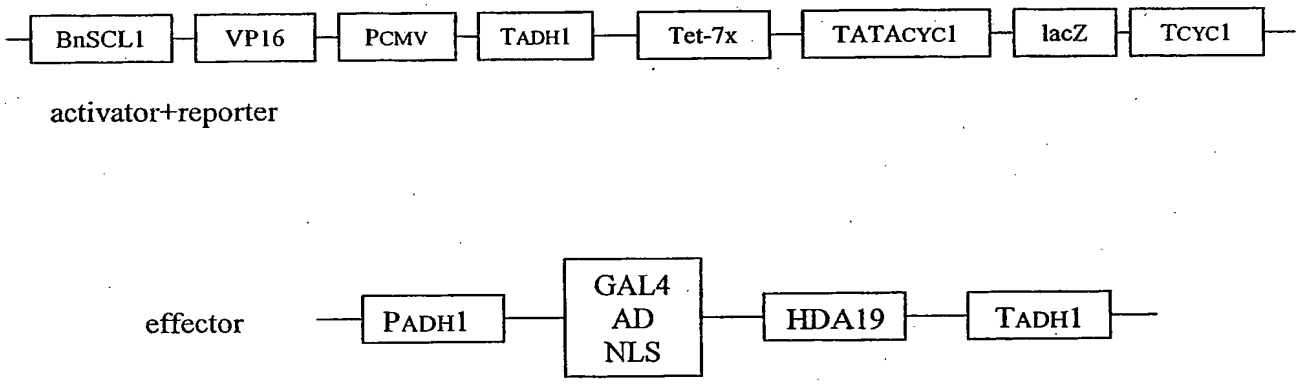


FIG. 29